RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/568,332
Source: IFW P
Date Processed by STIC: 2/27/06

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IFWP

RAW SEQUENCE LISTING DATE: 02/27/2006
PATENT APPLICATION: **US/10/568,332** TIME: 14:53:36

Input Set : **F:\61310.us.sequences.ST25.txt**
Output Set: **N:\CRF4\02272006\J568332.raw**

3 <110> APPLICANT: Stempfer, Gunter
4 Alliger, Peter
5 Palma, Norbert
7 <120> TITLE OF INVENTION: Process for the purification of recombinant polypeptides
9 <130> FILE REFERENCE: BP/G-33315A LNG 61310.US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/568,332
C--> 11 <141> CURRENT FILING DATE: 2006-02-13
11 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/009055
12 <151> PRIOR FILING DATE: 2004-08-12
14 <150> PRIOR APPLICATION NUMBER: US 60/494,915
15 <151> PRIOR FILING DATE: 2003-08-13
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 23
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Primer
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34 <211> LENGTH: 20
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial
38 <220> FEATURE:
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47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial
50 <220> FEATURE:
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58 <211> LENGTH: 19
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Primer

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69 <210> SEQ ID NO: 5
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71 <212> TYPE: PRT
72 <213> ORGANISM: Pseudomonas diminuta
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77 1 5 10 15
80 Val Ile Gly Leu Ala Pro Ala Val Ala Phe Ala
81 20 25
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 36
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Primer
92 <400> SEQUENCE: 6
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96 <210> SEQ ID NO: 7
97 <211> LENGTH: 32
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Primer
104 <400> SEQUENCE: 7
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109 <211> LENGTH: 315
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial
113 <220> FEATURE:
114 <223> OTHER INFORMATION: gac fragment
116 <400> SEQUENCE: 8
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119 ccgacctggg caatgggatg tacagcgggc ttgcgccgtt cggcttcacc ggcggatcct 120
121 ggttcgtacg cgccgcctac aagtggtgat ctaggggaac gttccggggg cgtcgctgca 180
123 acggcgtctc cggatctggg tgagagggga aatccatgct gagagttctg caccgggcgg 240
125 cgtccgcctt ggttatggcg actgtgatcg gccttgcgcc cgcggagaga gacgcgtact 300
127 agtgaattcg ggggg 315
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131 <211> LENGTH: 11
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Sac II site
138 <400> SEQUENCE: 9
139 tcgcctttgc g 11
142 <210> SEQ ID NO: 10

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<220> FEATURE:
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<211> LENGTH: 4
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: gac signal sequence
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<211> LENGTH: 540
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: Interferon alpha structural gene fragment
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gaaccttgat gcttctggca cagatgcggc gaatctctct tttctcttgc ttaaaggatc 120
gacatgactt cggtttcccg caggaggagt tcggtaacca gttccaaaag gctgaaacca 180
tcccggtatt gcatgagatg atccagcaga tcttcaacct gttcagcact aaggactctt 240
ctgctgcttg ggatgagacc ctgcttgaca aattctacac tgaactgtac cagcagctga 300
acgacctgga agcctgcgtg atccagggtg tgggtgtgac tgagactccg ctgatgaagg 360
aggactctat tctggctgtg cgaaaatact tccaacggat cactctgtat ctgaaagaga 420
agaaatacag cccgtgcgcc tgggaggttg tccgagcaga aatcatgcgg tctttctctt 480
tgtctaccaa cttgcaagaa tctttacgaa gcaaggaata atacgcgtga attcgggggg 540
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<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: gene encoding a gac1ss-rhIFNa2b fusion protein
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (210)..(788)
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tgggcaatgg gatgtacagc gggcttgcgc cgttcggctt caccggcgga tcctggttcg 120
tacgcgccgc ctacaagtgg tgatctaggg gaacgttccg ggggcgtcgc tgcaacggcg 180
tctccggatc tgggtgagag gggaaatcc atg ctg aga gtt ctg cac cgg gcg 233
Met Leu Arg Val Leu His Arg Ala
1 5
gcg tcc gcc ttg gtt atg gcg act gtg atc ggc ctt gcg ccc gcg gtc 281

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Input Set : F:\61310.us.sequences.ST25.txt
Output Set: N:\CRF4\02272006\J568332.raw

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221 Ala Ser Ala Leu Val Met Ala Thr Val Ile Gly Leu Ala Pro Ala Val
222     10                  15                  20
224 gcc ttt gcg tgc gat ctg ccg caa acc cac agc ctg ggt agc cgg cga      329
225 Ala Phe Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg
226 25                  30                  35                  40
228 acc ttg atg ctt ctg gca cag atg cgg cga atc tct ctt ttc tct tgc      377
229 Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys
230                 45                  50                  55
232 tta aag gat cga cat gac ttc ggt ttc ccg cag gag gag ttc ggt aac      425
233 Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn
234             60                  65                  70
236 cag ttc caa aag gct gaa acc atc ccg gta ttg cat gag atg atc cag      473
237 Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln
238         75                  80                  85
240 cag atc ttc aac ctg ttc agc act aag gac tct tct gct gct tgg gat      521
241 Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp
242     90                  95                  100
244 gag acc ctg ctt gac aaa ttc tac act gaa ctg tac cag cag ctg aac      569
245 Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn
246 105                 110                 115                 120
248 gac ctg gaa gcc tgc gtg atc cag ggt gtg ggt gtg act gag act ccg      617
249 Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro
250                 125                 130                 135
252 ctg atg aag gag gac tct att ctg gct gtg cga aaa tac ttc caa cgg      665
253 Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg
254             140                 145                 150
256 atc act ctg tat ctg aaa gag aag aaa tac agc ccg tgc gcc tgg gag      713
257 Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu
258         155                 160                 165
260 gtt gtc cga gca gaa atc atg cgg tct ttc tct ttg tct acc aac ttg      761
261 Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu
262     170                 175                 180
264 caa gaa tct tta cga agc aag gaa taa tacgcgtact agtgaattc            807
265 Gln Glu Ser Leu Arg Ser Lys Glu
266 185                 190
269 <210> SEQ ID NO: 14
270 <211> LENGTH: 192
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Synthetic Construct
277 <400> SEQUENCE: 14
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280 1               5                   10                  15
283 Val Ile Gly Leu Ala Pro Ala Val Ala Phe Ala Cys Asp Leu Pro Gln
284             20                  25                  30
287 Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met
288         35                  40                  45
291 Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly
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```
292     50                  55                  60
295 Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile
296 65                  70                  75                  80
299 Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
300                 85                  90                  95
303 Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr
304             100                 105                 110
307 Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln
308         115                 120                 125
311 Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu
312     130                 135                 140
315 Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys
316 145                 150                 155                 160
319 Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg
320                 165                 170                 175
323 Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
324             180                 185                 190
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY DATE: 02/27/2006
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date